

Additional file 9: Table S4. Completeness assessment of comprehensive transcript sequence sets of bony vertebrates based on numbers of detected genes

| Species ¹ | CEGMA referring to CEG | | | | CEGMA referring to CVG | | | | BUSCO referring to CVG ² | | | | BUSCO referring to the vertebrate set ² | | | |
|-----------------------------|------------------------|------------|-----------------|------------|------------------------|------------|-----------------|------------|-------------------------------------|------------|-----------------|------------|--|------------|-----------------|------------|
| | Complete | | Partial | | Complete | | Partial | | Complete | | Partial | | Complete | | Partial | |
| | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion | Number of genes | Proportion |
| | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes | of genes |
| <i>Pan troglodytes</i> | 230 | 0.9274 | 243 | 0.9798 | 220 | 0.9442 | 225 | 0.9657 | 222 | 0.953 | 225 | 0.966 | 2778 | 0.919 | 2818 | 0.932 |
| <i>Pongo abelii</i> | 227 | 0.9153 | 246 | 0.9919 | 217 | 0.9313 | 230 | 0.9871 | 225 | 0.966 | 228 | 0.979 | 2754 | 0.911 | 2848 | 0.942 |
| <i>Macaca mulatta</i> | 223 | 0.8992 | 240 | 0.9677 | 202 | 0.867 | 224 | 0.9614 | 219 | 0.940 | 226 | 0.970 | 2761 | 0.913 | 2907 | 0.962 |
| <i>Anas platyrhynchos</i> | 159 | 0.6411 | 200 | 0.8065 | 185 | 0.794 | 226 | 0.970 | 216 | 0.927 | 229 | 0.983 | 2304 | 0.762 | 2505 | 0.829 |
| <i>Meleagris gallopavo</i> | 161 | 0.6492 | 209 | 0.8427 | 181 | 0.7768 | 225 | 0.9657 | 221 | 0.948 | 228 | 0.979 | 2275 | 0.753 | 2463 | 0.815 |
| <i>Lepisosteus oculatus</i> | 210 | 0.8468 | 232 | 0.9355 | 221 | 0.9485 | 231 | 0.9914 | 228 | 0.979 | 232 | 0.996 | 2639 | 0.873 | 2714 | 0.898 |
| <i>Astyanax mexicanus</i> | 214 | 0.8629 | 239 | 0.9637 | 197 | 0.8455 | 221 | 0.9485 | 206 | 0.884 | 221 | 0.948 | 2434 | 0.805 | 2576 | 0.852 |
| <i>Takifugu rubripes</i> | 204 | 0.8226 | 244 | 0.9839 | 193 | 0.8283 | 218 | 0.9356 | 217 | 0.931 | 224 | 0.961 | 2616 | 0.865 | 2717 | 0.899 |

¹ Annotated transcript sequences were obtained from Ensembl version 75

² BUSCO run employed the ‘transcriptome’ mode.